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ser arg asn ile lau lys lau trp val trp thr lau lau cys cys asp phe lau ile his TCG AGG AAC ATC CTG GAG CTG TGG GTC TGG ACA CTG CTG [GT] TGT GAC TTC CTG ATA CAC M-Terminus 40
his gly the his [gys] trp the tyr his tyr ser glu lys pro met as rep glu sen ala
car gga acr cac [ter] rgg acr tac cat tat ter gaa aug ecc arg and rgg gaa and ger erg lye phe Cyr lye gin sen tyr thri sep leu val ala ile gin aen lye erg giu ile AGA AMG TTC TOO AMG CAA MAT TAC ACA GAT TTA GTC GCC ATA CAA AMC AMG AGA GAA ATT glo tyr leu glu asn thr leu pro lys ser pro tyr tyr tyr trp ile gly ile erg lys GAG TAT TTA GAG AAT ACA TTG CCC AAA ACC CCT TAT TAC TAG TTA GAG AAT AGA ATC AGG AAA 110 gly lys met trp thr trp val gly thr ash lys thr leu thr lys glu sia glu ash ATT GGG AAA ATG TGG ACA TGG GTG GGA ACC LAG AAA ACT CTC ACT AAA GAA GCA GAG AAC trp gly alm gly glu pro san man lys lys mer lys glu map [cys] val glu ile tyr ile Toc get eet eeg eag eee aac aac aag aag tee aag eag eeg gra val glu ile tyr ile leu Eye tyr the als ser feye gin pro gly ser feye asn gly arg gly giu Eye vai glu cre rec tec the ACA occ ter tres can con ter tres AAT occ cot can GAN TEST CTG GAN the ile sen sen his the sys lie cys asp ale gly tye tyr gly pro sin Cys gin tye Act Arc Acc CAC Cyc) are tigg GAT GCA GGG TAT TAC GGG CCC CAG [GCT] CAG TAT val val qin cya qiu pro lau qiu ala pro qiu lau qiy thr met asp cya ila his pro cre cre case ison case cor tre case cor cre case tre case case ison case core leu gly man phe sen phe gin ser lys Eys ala phe man Eys as glu gly acg glu lev TTG GGA AAC TTC ACC TTC CAG TCC AAG TEEL CCT TTC BAC LIGHT TCT GAG GGA AGA GAG CTA 240 250 leu gly thr sla glu thr gin CYP gly ala ser gly man trp ser ser pro glu pro ile CTT GGG ACT GCA GAA ACA CAG TGGT GGA GCA TCT GGA AAC TGG TCA TCT CCA GAG CCA ATC CYA gin val val gin CYA giu pro leu glu ela pro glu leu gly thr met asp CYA lec CAA GTG GTC CAG TGT GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC TCC ATC 280
his pro leu gly san phe seri phe gln ser lye Gys ale phe sen Gys seri glu gly arg
CMC CCC TTG GGA AAAC TTG AGG TTG CAG TCC AAG TGT GCT TTG AAC TGT TCT GAG GGA AGA glu leu leu qly thr ala glu thr qln [cya] gly ala ser gly ain tip set ser pro glu GAG CTA CTT GGG ACT GGA GAA ACA CAG [TC] GGA GGA TCT GGA AAC TGG TCA TCT CCA GAG TTTTACACGCAGGCATCTCCCACATTAGAGATGCAGTGTTTGCTCAACGAATCTGGAAGGATTTCTTCATGACG ITATTAATAGTTAATGATAACACAACCCACTCTCTTGGAGCTGATGTTATGAAGACAACAGGTAGAAAAATTC et cagget ggagt gacaccett ti et ti ecet aacateti et acteagat acet aaat ti aagati caggaca TGTCCCCAACTCTTACCATGTCTTTTATAACTTGCTCCTTAACTTGCCCAACCTGTAGGCTATCTCATTTTCTCCC 

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ENARKFCKONYTOLVA! ONKRE! EYKENTLPKSPYYYNI GIRKI GKMWTW ORARRECRDNYTOLVA! ONKAE! EYKEKTLPFSRSYYWI GIRKI GGI WTW V GT NKTL TKE A E N WGAGE P N N KKSKE D C V E I Y I KRE RDSGK WN D DA CHKR V GT N KSLTEE A E N WGDGE P N N KKN K G O C V E I Y I KRN KDAGK WN D DA CHKL KAALCYTASCOPWSCSCHGECVETINNHTCHCOVGYYGPOCGYUVOCEPL MI FPWRGEGTY WGS ANILK LWVWTLL CODFLI HHGTHCWTY HYSEKPMNIMI FRLWGWTML CCOFLAHHGTYCWTY HYSEKPMNI EAPELGTMDCIHPLGNFSFOSKCAFNCSEGRELLGTAETOCGASGNWSSPEAPELGTMDCTHPFGNFSFSSOCAFSCSEGTNLTGIEETTCGPFGNWSSP EPI COVVOCEPLEAPELGTMOCI HPLANFSFOSKCAFNCSEGRELLGTAE Transmembrane Domain Complement Binding Repeat 1 Complement Binding Repeat 2 Lectin Domain Signal Sequence MLHR HLHR MLHR HLHR MLHK HLHR MLHR HLHR MLHR MLHR HLHR

Cytoplasmic Domain —

TOCGASGNWSSPEPICOETNRSFSKIKEGDYNPLF: PVAVMVTAFSGLAF TIGESSGIWSNPSPICOKLDKSFSMIKEGDYNPLFIPVAVMVTAFSGLAF

M.HR HLHR MLHR I WLARRLKKGKKSOERMDDPY HLHR I WLARRLKKGKKSKRSMNOPY

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MW (Kd)
—— 200
—— 116
—— 93
—— 66

- 45

FIG.4A

Fig. 4 B

K M KF K V<u>VIL</u> K
10 20 30
EKPMNWENARKFXKQNYTDLVAIQNKXXIEYL

Fig. 4c

A C A C A C AAG CCC ATG AAT TGG GAG AAT GC 3'

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A B C D E F MW (Kd)

- 200

- 97

- 68

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1 WASTW.  1 SCYWFSS VK PW TEADLACGTV HPGARY LATI OSOLENAF: SETVSNN  1 SCYWFSS VK PW TEADLACGTV HPGARY LATI OSOLENAF: SETVSNN  2 SISCYWFSS VK PW TEADLACGE ENAH LINVV TSWEEGRFVOOHM O  2 SCYWFSRDOL TWAEAPACD MEGO LVSI HSPEEOFFT KHASHTR  2 SISCYWFSRDOL TWAEAPACD MEGO LVSI HSPEEOFFT KHASHTR  3 SCYWFSRDOL TWAEAADOY COMEIAH LLVI NSREEOFFV K HRG  1 Y CYYF MEDHLSWAEADLF CONMNSGY LSOAEGNFLASLIKES  2 SCYWFSRDOK SWHEAL CSE RG TVAI PKNAEENKAI OEVAKT  2 KFY TSRDK SWHEAENFCOAHDOO LVSI PKNAEENKAI OEVAKT  2 KFY FSRDK SWHEAECAHDOO LVSV TSOEEOFFLV O TN  2 KFY FSRDK SWHEAECAHDOO LVSV TSOEEOFFLV O TN  2 KF TSTNGOS VNFDAIREVCAHAGGR AVP RSLEENEA	4	
Barn.Lec Ra.Heplec Ch.Heplec Ch.Heplec Hu.IgERec Ra.ASCRec Ra.ARP Ra.HEDA	Drickamer MLIIR Hu.Heplec Barn.Lec Ra.Heplec Hb.19ERec Hb.19ERec Ha.18ER Ra.18ER Ra.18ER Ra.18ER Ra.18ER Ra.18ER Ra.18ER Ra.18ER Ra.18EP Ra.18EP Ch.18EP Ch.18EP Ra.18EP Ra.18	

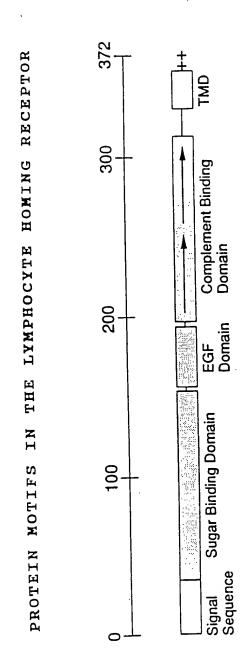
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